

SEQUENCE LISTING

<110> Greene, John M.
Fleischmann, Robert D.
Ni, Jian

<120> Human Tumor Necrosis Factor Receptor-Like Genes

<130> 1488.0710005

<140>

<141>

<160> 11

<170> PatentIn Ver. 2.0

<210> 1

<211> 1527

<212> DNA

<213> Homo sapiens

<220>

<221> sig_peptide

<222> (46)..(106)

<220>

<221> mat_peptide

<222> (109)..(1248)

<220>

<221> CDS

<222> (46)..(1248)

<400> 1

cgcccagccg ccgcctccaa gccctgagg tttccgggga ccaca atg aac aag ttg 57

Met Asn Lys Leu

-20

ctg tgc tgc gcg ctc gtg ttt ctg gac atc tcc att aag tgg acc acc 105

Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr

-15

-10

-5

cag gaa acg ttt cct cca aag tac ctt cat tat gac gaa gaa acc tct 153

Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser

-1 1

5

10

15

cat cag ctg ttg tgt gac aaa tgt cct cct ggt acc tac cta aaa caa 201

His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln

20

25

30

cac tgt aca gca aag tgg aag acc gtg tgc gcc cct tgc cct gac cac 249

His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	Cys	Pro	Asp	His	
			35					40					45			
tac	tac	aca	gac	agc	tgg	cac	acc	agt	gac	gag	tgt	cta	tac	tgc	agc	297
Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	
		50					55					60				
ccc	gtg	tgc	aag	gag	ctg	cag	tac	gtc	aag	cag	gag	tgc	aat	cgc	acc	345
Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	
	65					70					75					
cac	aac	cgc	gtg	tgc	gaa	tgc	aag	gaa	ggg	cgc	tac	ctt	gag	ata	gag	393
His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	
	80				85				90						95	
ttc	tgc	ttg	aaa	cat	agg	agc	tgc	cct	cct	gga	ttt	gga	gtg	gtg	caa	441
Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	
			100					105					110			
gct	gga	acc	cca	gag	cga	aat	aca	gtt	tgc	aaa	aga	tgt	cca	gat	ggg	489
Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	
		115					120						125			
ttc	ttc	tca	aat	gag	acg	tca	tct	aaa	gca	ccc	tgt	aga	aaa	cac	aca	537
Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	
		130					135					140				
aat	tgc	agt	gtc	ttt	ggt	ctc	ctg	cta	act	cag	aaa	gga	aat	gca	aca	585
Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	
	145					150				155						
cac	gac	aac	ata	tgt	tcc	gga	aac	agt	gaa	tca	act	caa	aaa	tgt	gga	633
His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	
	160				165				170						175	
ata	gat	gtt	acc	ctg	tgt	gag	gag	gca	ttc	ttc	agg	ttt	gct	gtt	cct	681
Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	
			180					185					190			
aca	aag	ttt	acg	cct	aac	tgg	ctt	agt	gtc	ttg	gta	gac	aat	ttg	cct	729
Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	
		195					200						205			
ggc	acc	aaa	gta	aac	gca	gag	agt	gta	gag	agg	ata	aaa	cgg	caa	cac	777
Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	
	210					215						220				
agc	tca	caa	gaa	cag	act	ttc	cag	ctg	ctg	aag	tta	tgg	aaa	cat	caa	825
Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	
	225					230					235					
aac	aaa	gac	caa	gat	ata	gtc	aag	aag	atc	atc	caa	gat	att	gac	ctc	873

00526437-034500

Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu	
240 245 250 255	
tgt gaa aac agc gtg cag cgg cac att gga cat gct aac ctc acc ttc	921
Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe	
260 265 270	
gag cag ctt cgt agc ttg atg gaa agc tta ccg gga aag aaa gtg gga	969
Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly	
275 280 285	
gca gaa gac att gaa aaa aca ata aag gca tgc aaa ccc agt gac cag	1017
Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln	
290 295 300	
atc ctg aag ctg ctc agt ttg tgg cga ata aaa aat ggc gac caa gac	1065
Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp	
305 310 315	
acc ttg aag ggc cta atg cac gca cta aag cac tca aag acg tac cac	1113
Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His	
320 325 330 335	
ttt ccc aaa act gtc act cag agt cta aag aag acc atc agg ttc ctt	1161
Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu	
340 345 350	
cac agc ttc aca atg tac aaa ttg tat cag aag tta ttt tta gaa atg	1209
His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met	
355 360 365	
ata ggt aac cag gtc caa tca gta aaa ata agc tgc tta taactggaaa	1258
Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu	
370 375 380	
tggccattga gctgtttcct cacaattggc gagatcccat ggatgagtaa actgtttctc	1318
aggcacttga ggctttcagt gatattcttc tcattaccag tgactaattt tgccacaggg	1378
tactaaaaga aactatgatg tggagaaagg actaacatct cctccaataa accccaaatg	1438
gttaatccaa ctgtcagatc tggatcgta tctactgact atattttccc ttattactgc	1498
ttgcagtaat tcaactggaa aaaaaaaaaa	1527

<210> 2

<211> 401

<212> PRT

<213> Homo sapiens

<400> 2

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5 -1 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
30 35 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
160 165 170

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
175 180 185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
190 195 200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
205 210 215

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
220 225 230 235

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln
240 245 250

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala

265

Leu
380

```
<210> 3
<211> 1188
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> sig_peptide  
<222> (1)..(61)
```

```
<220>  
<221> mat_peptide  
<222> (64)..(1185)
```

```
<220>  
<221> CDS  
<222> (1) .. (1185)
```

```
<400> 3
atg aac aag ttg ctg tgc tgc gcg ctc gtg ttt ctg gac atc tcc att    48
Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
      -20                -15                -10
```

aag tgg acc acc cag gaa acg ttt cct cca aag tac ctt cat tat gac 96
Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5 -1 1 5 10

gaa	gaa	acc	tct	cat	cag	ctg	ttg	tgt	gac	aaa	tgt	cct	cct	ggg	acc	144
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15			20						25				
tac	cta	aaa	caa	cac	tgt	aca	gca	aag	tgg	aag	acc	gtg	tgc	gcc	cct	192
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	
			30			35						40				
tgc	cct	gac	cac	tac	tac	aca	gac	agc	tgg	cac	acc	agt	gac	gag	tgt	240
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
			45			50						55				
cta	tac	tgc	agc	ccc	gtg	tgc	aag	gag	ctg	cag	tac	gtc	aag	cag	gag	288
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	
60			65			70						75				
tgc	aat	cgc	acc	cac	aac	cgc	gtg	tgc	gaa	tgc	aag	gaa	ggg	cgc	tac	336
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	
			80			85						90				
ctt	gag	ata	gag	ttc	tgc	ttg	aaa	cat	agg	agc	tgc	cct	cct	gga	ttt	384
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	
			95			100						105				
gga	gtg	gtg	caa	gct	gga	acc	cca	gag	cga	aat	aca	gtt	tgc	aaa	aga	432
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	
			110			115						120				
tgt	cca	gat	ggg	ttc	ttc	tca	aat	gag	acg	tca	tct	aaa	gca	ccc	tgt	480
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	
			125			130						135				
aga	aaa	cac	aca	aat	tgc	agt	gtc	ttt	ggg	ctc	ctg	cta	act	cag	aaa	528
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	
140			145			150						155				
gga	aat	gca	aca	cac	gac	aac	ata	tgt	tcc	gga	aac	agt	gaa	tca	act	576
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	
			160			165						170				
caa	aaa	tgt	gga	ata	gat	gtt	acc	ctg	tgt	gag	gag	gca	ttc	ttc	agg	624
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	
			175			180						185				
ttt	gct	gtt	cct	aca	aag	ttt	acg	cct	aac	tgg	ctt	agt	gtc	ttg	gta	672
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	
			190			195						200				
gac	aat	ttg	cct	ggc	acc	aaa	gta	aac	gca	gag	agt	gta	gag	agg	ata	720
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	
			205			210						215				

aaa cgg caa cac agc tca caa gaa cag act ttc cag ctg ctg aag tta	768
Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu	
220 225 230 235	
tggtg aaa cat caa aac aaa gac caa gat ata gtc aag aag atc atc caa	816
Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln	
240 245 250	
gat att gac ctc tgt gaa aac agc gtg cag cgg cac att gga cat gct	864
Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala	
255 260 265	
aac ctc acc ttc gag cag ctt cgt agc ttg atg gaa agc tta ccg gga	912
Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly	
270 275 280	
aag aaa gtg gga gca gaa gac att gaa aaa aca ata aag gca tgc aaa	960
Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys	
285 290 295	
ccc agt gac cag atc ctg aag ctg ctc agt ttg tgg cga ata aaa aat	1008
Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn	
300 305 310 315	
ggc gac caa gac acc ttg aag ggc cta atg cac gca cta aag cac tca	1056
Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser	
320 325 330	
aag acg tac cac ttt ccc aaa act gtc act cag agt cta aag aag acc	1104
Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr	
335 340 345	
atc agg ttc ctt cac agc ttc aca atg tac aaa ttg tat cag aag tta	1152
Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu	
350 355 360	
ttt tta gaa atg ata ggt aat cta gaa aag atc taa	1188
Phe Leu Glu Met Ile Gly Asn Leu Glu Lys Ile	
365 370	

<210> 4

<211> 395

<212> PRT

<213> Homo sapiens

<400> 4

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp

-5			-1			1			5			10			
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr
			15						20			25			
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro
			30			35						40			
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys
45						50						55			
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu
60			65						70			75			
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr
			80						85			90			
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe
			95			100						105			
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg
110						115						120			
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys
125						130			135						
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys
140			145						150			155			
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr
			160						165			170			
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg
			175			180						185			
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val
190						195						200			
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile
205						210			215						
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu
220			225						230			235			
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln
			240						245			250			
Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala
			255			260						265			
Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly
270						275						280			

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
285 290 295

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
300 305 310 315

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
320 325 330

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
335 340 345

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
350 355 360

Phe Leu Glu Met Ile Gly Asn Leu Glu Lys Ile
365 370

<210> 5

<211> 461

<212> PRT

<213> Homo sapiens

<400> 5

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140

Pro 145	Gly	Phe	Gly	Val	Ala	Arg	Pro	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val 160
Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr 175
Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly 180
Asn	Ala	Ser	Met	Asp	Ala	Val	Cys	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser 195
Met	Ala	Pro	Gly	Ala	Val	His	Leu	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser 210
Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser 225
Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly 240
Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	Ile	Val	Gly	Val	Thr	Ala	Leu	Gly 255
Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	Cys	Val	Ile	Met	Thr	Gln	Val	Lys 270
Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	Glu	Ala	Lys	Val	Pro	His	Leu	Pro 285
Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln	Gly	Pro	Glu	Gln	Gln	His	Leu	Leu 300
Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Glu	Ser	Ser	Ala	Ser 315
Ala	Leu	Asp	Arg	Arg	Ala	Pro	Thr	Arg	Asn	Gln	Pro	Gln	Ala	Pro	Gly 330
Val	Glu	Ala	Ser	Gly	Ala	Gly	Glu	Ala	Arg	Ala	Ser	Thr	Gly	Ser	Ser 345
Asp	Ser	Ser	Pro	Gly	Gly	His	Gly	Thr	Gln	Val	Asn	Val	Thr	Cys	Ile 360
Val	Asn	Val	Cys	Ser	Ser	Ser	Asp	His	Ser	Ser	Gln	Cys	Ser	Ser	Gln 375
Ala	Ser	Ser	Thr	Met	Gly	Asp	Thr	Asp	Ser	Ser	Pro	Ser	Glu	Ser	Pro 400

```
<210> 10
<211> 31
<212> DNA
<213> Homo sapiens

<400> 10
```

31

<213> Homo sapiens

gcgctctaga ttacctatca tttctaaaaa taac

34